

10/530217

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SEQUENCE LISTING

<110> Nakamura, Yusuke
Katagiri, Toyomasa

<120> GENES AND POLYPEPTIDES RELATING TO HUMAN
MYELOID LEUKEMIA

<130> 082368-003910US

<150> PCT/JP03/09589

<151> 2003-07-29

<150> US 60/414,867

<151> 2002-09-30

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Met Ser
1

gag gcc cgc agg gac agc acg agc agc ctg cag cgc aag aag cca ccc 164
Glu Ala Arg Arg Asp Ser Thr Ser Ser Leu Gln Arg Lys Lys Pro Pro
5 10 15

tgg cta aag ctg gac att ccc tct gcg gtg ccc ctg acg gca gaa gag 212
Trp Leu Lys Leu Asp Ile Pro Ser Ala Val Pro Leu Thr Ala Glu Glu
20 25 30

ccc agc ttc ctg cag ccc ctg agg cga cag gct ttc ctg agg agt gtg 260
Pro Ser Phe Leu Gln Pro Leu Arg Arg Gln Ala Phe Leu Arg Ser Val
35 40 45 50

agt atg cca gcc gag aca gcc cac atc tct tca ccc cac cat gag ctc 308
Ser Met Pro Ala Glu Thr Ala His Ile Ser Ser Pro His His Glu Leu
55 60 65

cgg cgg ccg gtg ctg caa cgc cag acg tcc atc aca cag acc atc cgc 356
Arg Arg Pro Val Leu Gln Arg Gln Thr Ser Ile Thr Gln Thr Ile Arg
70 75 80

agg ggg acc gcc gag aca gcc cac atc tct tca ccc cac cat gag ctc 404
Arg Gly Thr Ala Asp Trp Phe Gly Val Ser Lys Asp Ser Asp Ser Thr
85 90 95

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Gln Lys Trp Gln Arg Lys Ser Ile Arg His Cys Ser Gln Arg Tyr Gly
100 105 110

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Lys Leu Lys Pro Gln Val Leu Arg Glu Leu Asp Leu Pro Ser Gln Asp
115 120 125 130

aac gtg tgc ctg acc agc acc gag acg cca ccc cca ctc tac gtg ggg 548
Asn Val Ser Leu Thr Ser Thr Glu Thr Pro Pro Pro Leu Tyr Val Gly
135 140 145

cca tgc cag ctg ggc atg cag aag atc ata gac ccc ctg gcc cgt ggc 596
Pro Cys Gln Leu Gly Met Gln Lys Ile Ile Asp Pro Leu Ala Arg Gly
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cgt gcc ttc cgt gtg gca gat gac act gcg gaa ggc ctg agt gcc cca 644

405					410					415						
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Ile	Leu	Ala	Val	Cys	Ile	Tyr	Gly	Ile	Ala	Pro	Val	Gly	Phe	Ser	Gln	
	420					425					430					
cat	gag	acg	gtg	gac	tcg	gtg	ctg	cgg	aac	cgc	ggg	gtc	tac	gag	aac	1460
His	Glu	Thr	Val	Asp	Ser	Val	Leu	Arg	Asn	Arg	Gly	Val	Tyr	Glu	Asn	
	435					440				445					450	
gtc	aag	tac	gtg	cag	cag	gag	aac	ttc	tgg	atc	ggg	ccc	agc	tcg	gag	1508
Val	Lys	Tyr	Val	Gln	Gln	Glu	Asn	Phe	Trp	Ile	Gly	Pro	Ser	Ser	Glu	
				455					460						465	
gcc	ctc	atc	cac	ctg	ggc	gcc	aag	ttt	tcg	ccc	tgc	atg	cgc	cag	gac	1556
Ala	Leu	Ile	His	Leu	Gly	Ala	Lys	Phe	Ser	Pro	Cys	Met	Arg	Gln	Asp	
			470					475						480		
ccg	cag	gtg	cac	agc	ttc	att	cgc	tcg	gcg	cgc	gag	cgc	gag	aag	cac	1604
Pro	Gln	Val	His	Ser	Phe	Ile	Arg	Ser	Ala	Arg	Glu	Arg	Glu	Lys	His	
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Ser	Ala	Cys	Cys	Val	Arg	Asn	Asp	Arg	Ser	Gly	Cys	Val	Gln	Thr	Ser	
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gag	gag	gag	tgc	tcg	tcc	acg	ctg	gca	gtg	tgg	gtg	aag	tgg	ccc	atc	1700
Glu	Glu	Glu	Cys	Ser	Ser	Thr	Leu	Ala	Val	Trp	Val	Lys	Trp	Pro	Ile	
	515					520				525					530	
cat	ccc	agc	gcc	cca	gag	ctt	gcg	ggc	cac	aag	aga	cag	ttt	ggc	tct	1748
His	Pro	Ser	Ala	Pro	Glu	Leu	Ala	Gly	His	Lys	Arg	Gln	Phe	Gly	Ser	
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gtc	tgc	cac	cag	gat	ccc	agg	gtg	tgt	gat	gag	ccc	tcc	tcc	gaa	gac	1796
Val	Cys	His	Gln	Asp	Pro	Arg	Val	Cys	Asp	Glu	Pro	Ser	Ser	Glu	Asp	
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cct	cat	gag	tgg	cca	gaa	gac	atc	acc	aag	tgg	ccg	atc	tgc	acc	aaa	1844
Pro	His	Glu	Trp	Pro	Glu	Asp	Ile	Thr	Lys	Trp	Pro	Ile	Cys	Thr	Lys	
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aac	agc	gct	ggg	aac	cac	acc	aac	cat	ccc	cac	atg	gac	tgt	gtc	atc	1892
Asn	Ser	Ala	Gly	Asn	His	Thr	Asn	His	Pro	His	Met	Asp	Cys	Val	Ile	
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aca	gga	cgg	ccc	tgc	tgc	att	ggc	acc	aag	ggc	agg	tgt	gag	atc	acc	1940
Thr	Gly	Arg	Pro	Cys	Cys	Ile	Gly	Thr	Lys	Gly	Arg	Cys	Glu	Ile	Thr	
	595				600					605					610	
tcc	cgg	gag	tac	tgt	gac	ttc	atg	agg	ggc	tac	ttc	cat	gag	gag	gcc	1988
Ser	Arg	Glu	Tyr	Cys	Asp	Phe	Met	Arg	Gly	Tyr	Phe	His	Glu	Glu	Ala	
				615					620						625	
acg	ctc	tgc	tct	cag	gtg	cac	tgc	atg	gat	gat	gtg	tgt	ggg	ctc	ctg	2036
Thr	Leu	Cys	Ser	Gln	Val	His	Cys	Met	Asp	Asp	Val	Cys	Gly	Leu	Leu	
			630					635					640			
cct	ttt	ctc	aac	ccc	gag	gtg	cct	gac	cag	ttc	tac	cgc	ctg	tgg	cta	2084
Pro	Phe	Leu	Asn	Pro	Glu	Val	Pro	Asp	Gln	Phe	Tyr	Arg	Leu	Trp	Leu	
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Ser Leu Phe Leu His Ala Gly Ile Leu His Cys Leu Val Ser Ile Cys	
660 665 670	
ttc cag atg act gtc ctg cgg gac ctg gag aag ctg gca ggc tgg cac	2180
Phe Gln Met Thr Val Leu Arg Asp Leu Glu Lys Leu Ala Gly Trp His	
675 680 685 690	
cgc ata gcc atc atc tac ctg ctg agt ggt gtc acc ggc aac ctg gcc	2228
Arg Ile Ala Ile Ile Tyr Leu Leu Ser Gly Val Thr Gly Asn Leu Ala	
695 700 705	
agt gcc atc ttc ctg cca tac cga gca gag gtg ggt cct gct ggc tcc	2276
Ser Ala Ile Phe Leu Pro Tyr Arg Ala Glu Val Gly Pro Ala Gly Ser	
710 715 720	
cag ttc ggc atc ctg gcc tgc ctc ttc gtg gag ctc ttc cag agc tgg	2324
Gln Phe Gly Ile Leu Ala Cys Leu Phe Val Glu Leu Phe Gln Ser Trp	
725 730 735	
cag atc ctg gcg cgg ccc tgg cgt gcc ttc ttc aag ctg ctg gct gtg	2372
Gln Ile Leu Ala Arg Pro Trp Arg Ala Phe Phe Lys Leu Leu Ala Val	
740 745 750	
gtg ctc ttc ctc ttc acc ttt ggg ctg ctg ccg tgg att gac aac ttt	2420
Val Leu Phe Leu Phe Thr Phe Gly Leu Leu Pro Trp Ile Asp Asn Phe	
755 760 765 770	
gcc cac atc tcg ggg ttc atc agt ggc ctc ttc ctc tcc ttc gcc ttc	2468
Ala His Ile Ser Gly Phe Ile Ser Gly Leu Phe Leu Ser Phe Ala Phe	
775 780 785	
ttg ccc tac atc agc ttt ggc aag ttc gac ctg tac cgg aaa cgc tgc	2516
Leu Pro Tyr Ile Ser Phe Gly Lys Phe Asp Leu Tyr Arg Lys Arg Cys	
790 795 800	
cag atc atc atc ttt cag gtg gtc ttc ctg ggc ctc ctg gct ggc ctg	2564
Gln Ile Ile Ile Phe Gln Val Val Phe Leu Gly Leu Leu Ala Gly Leu	
805 810 815	
gtg gtc ctc ttc tac gtc tat cct gtc cgc tgt gag tgg tgt gag ttc	2612
Val Val Leu Phe Tyr Val Tyr Pro Val Arg Cys Glu Trp Cys Glu Phe	
820 825 830	
ctc acc tgc atc ccc ttc act gac aag ttc tgt gag aag tac gaa ctg	2660
Leu Thr Cys Ile Pro Phe Thr Asp Lys Phe Cys Glu Lys Tyr Glu Leu	
835 840 845 850	
gac gct cag ctc cac tga gctggctgcg ggctccagcg gccgtgtgct	2708
Asp Ala Gln Leu His *	
855	
ccagcaggcc agagccagac acgacctccc tgagcctcac aggcttacag gagtcacctg	2768
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cattaacttg	2958

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Glu	Glu	Pro	Ser	Phe	Leu	Gln	Pro	Leu	Arg	Arg	Gln	Ala	Phe	Leu	Arg
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Ser	Val	Ser	Met	Pro	Ala	Glu	Thr	Ala	His	Ile	Ser	Ser	Pro	His	His
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Glu	Leu	Arg	Arg	Pro	Val	Leu	Gln	Arg	Gln	Thr	Ser	Ile	Thr	Gln	Thr
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Ile	Arg	Arg	Gly	Thr	Ala	Asp	Trp	Phe	Gly	Val	Ser	Lys	Asp	Ser	Asp
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Tyr	Gly	Lys	Leu	Lys	Pro	Gln	Val	Leu	Arg	Glu	Leu	Asp	Leu	Pro	Ser
		115					120					125			
Gln	Asp	Asn	Val	Ser	Leu	Thr	Ser	Thr	Glu	Thr	Pro	Pro	Pro	Leu	Tyr
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Arg	Gly	Arg	Ala	Phe	Arg	Val	Ala	Asp	Asp	Thr	Ala	Glu	Gly	Leu	Ser
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Ala	Pro	His	Thr	Pro	Val	Thr	Pro	Gly	Ala	Ala	Ser	Leu	Cys	Ser	Phe
			180					185					190		
Ser	Ser	Ser	Arg	Ser	Gly	Phe	His	Arg	Leu	Pro	Arg	Arg	Arg	Lys	Arg
		195					200					205			
Glu	Ser	Val	Ala	Lys	Met	Ser	Phe	Arg	Ala	Ala	Ala	Ala	Leu	Met	Lys
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Gly	Arg	Ser	Val	Arg	Asp	Gly	Thr	Phe	Arg	Arg	Ala	Arg	Arg	Arg	Ser
225					230					235					240
Phe	Thr	Pro	Ala	Ser	Phe	Leu	Glu	Glu	Asp	Thr	Thr	Asp	Phe	Pro	Asp
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Glu	Leu	Asp	Thr	Ser	Phe	Phe	Ala	Arg	Glu	Gly	Ile	Leu	His	Glu	Glu
			260						265				270		
Leu	Ser	Thr	Tyr	Pro	Asp	Glu	Val	Phe	Glu	Ser	Pro	Ser	Glu	Ala	Ala
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Leu	Lys	Asp	Trp	Glu	Lys	Ala	Pro	Glu	Gln	Ala	Asp	Leu	Thr	Gly	Gly
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Ala	Leu	Asp	Arg	Ser	Glu	Leu	Glu	Arg	Ser	His	Leu	Met	Leu	Pro	Leu
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Glu	Arg	Gly	Trp	Arg	Lys	Gln	Lys	Glu	Gly	Ala	Ala	Ala	Pro	Gln	Pro
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Lys	Val	Arg	Leu	Arg	Gln	Glu	Val	Val	Ser	Thr	Ala	Gly	Pro	Arg	Arg
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Asp	His	Arg	Pro	Phe	Phe	Thr	Tyr	Trp	Leu	Thr	Phe	Val	His	Ser	Leu
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Gln	Asp	Pro	Gln	Val	His	Ser	Phe	Ile	Arg	Ser	Ala	Arg	Glu	Arg	Glu	485	490	495
Lys	His	Ser	Ala	Cys	Cys	Val	Arg	Asn	Asp	Arg	Ser	Gly	Cys	Val	Gln	500	505	510
Thr	Ser	Glu	Glu	Glu	Cys	Ser	Ser	Thr	Leu	Ala	Val	Trp	Val	Lys	Trp	515	520	525
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Gly	Ser	Val	Cys	His	Gln	Asp	Pro	Arg	Val	Cys	Asp	Glu	Pro	Ser	Ser	545	550	555
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Thr	Lys	Asn	Ser	Ala	Gly	Asn	His	Thr	Asn	His	Pro	His	Met	Asp	Cys	580	585	590
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Ile	Thr	Ser	Arg	Glu	Tyr	Cys	Asp	Phe	Met	Arg	Gly	Tyr	Phe	His	Glu	610	615	620
Glu	Ala	Thr	Leu	Cys	Ser	Gln	Val	His	Cys	Met	Asp	Asp	Val	Cys	Gly	625	630	635
Leu	Leu	Pro	Phe	Leu	Asn	Pro	Glu	Val	Pro	Asp	Gln	Phe	Tyr	Arg	Leu	645	650	655
Trp	Leu	Ser	Leu	Phe	Leu	His	Ala	Gly	Ile	Leu	His	Cys	Leu	Val	Ser	660	665	670
Ile	Cys	Phe	Gln	Met	Thr	Val	Leu	Arg	Asp	Leu	Glu	Lys	Leu	Ala	Gly	675	680	685
Trp	His	Arg	Ile	Ala	Ile	Ile	Tyr	Leu	Leu	Ser	Gly	Val	Thr	Gly	Asn	690	695	700
Leu	Ala	Ser	Ala	Ile	Phe	Leu	Pro	Tyr	Arg	Ala	Glu	Val	Gly	Pro	Ala	705	710	715
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Ser	Trp	Gln	Ile	Leu	Ala	Arg	Pro	Trp	Arg	Ala	Phe	Phe	Lys	Leu	Leu	740	745	750
Ala	Val	Val	Leu	Phe	Leu	Phe	Thr	Phe	Gly	Leu	Leu	Pro	Trp	Ile	Asp	755	760	765
Asn	Phe	Ala	His	Ile	Ser	Gly	Phe	Ile	Ser	Gly	Leu	Phe	Leu	Ser	Phe	770	775	780
Ala	Phe	Leu	Pro	Tyr	Ile	Ser	Phe	Gly	Lys	Phe	Asp	Leu	Tyr	Arg	Lys	785	790	795
Arg	Cys	Gln	Ile	Ile	Phe	Gln	Val	Val	Phe	Leu	Gly	Leu	Leu	Ala		805	810	815
Gly	Leu	Val	Val	Leu	Phe	Tyr	Val	Tyr	Pro	Val	Arg	Cys	Glu	Trp	Cys	820	825	830
Glu	Phe	Leu	Thr	Cys	Ile	Pro	Phe	Thr	Asp	Lys	Phe	Cys	Glu	Lys	Tyr	835	840	845
Glu	Leu	Asp	Ala	Gln	Leu	His										850	855	